

# FIGURE 1

GGCTGAGGGGAGGCCCCGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGA  
GAGAAGCGCCTGCAGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCCTCTGGCGGCATGTAA  
AGGCTCCACAAAGGAGTTGGGAGTTCAAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCC  
CAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGGCTGACGCTACTGTGAGGGAAAGA  
AGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTGCCGGAGCCCT  
CTGTGGAGGCAGAGCCAGTGGAGCCCAGTGGAGGAGGCTGCTTGCGAGCCACCGGCCTGCA  
ACTCAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCGCTGACGGCCAGGGTGAAGCATG  
TGAGGAGCCGCCCCGGAGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGA  
ATAACCACCATTTTGAAGGACC**ATG**AGGCCACTGTGCGTGACATGCTGGTGGCTCGGACTG  
CTGGCTGCCATGGGAGCTGTTGACAGGCCAGGAGGACGGTTTTTGAGGGCACTGAGGAGGGCTC  
GCCAAGAGAGTTTCAATTTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCAGGACAAGTGCA  
CCTACACCTTCATTGTGCCCCAGCAGCGGGTCACGGGTGCCATCTGCGTCAACTCCAAGGAG  
CCTGAGGTGCTTCTGGAGAACCAGTGCA**T**AAGCAGGAGCTAGAGCTGCTCAACAATGAGCT  
GCTCAAGCAGAAGCGGCAGATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTG  
TGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGCCGCAACATGAACTCGCGGGTCACGCAGCTC  
TACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCGTTGGAGCTCTCCCAGCT  
GGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAGGACC  
TGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCCACAACCAATCAGAGATCATCGCGCAG  
CTTGAGGAGCACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCCAGCCACCCCCCGCTGC  
CCCGCCCCGGGTCTACCAACCACCCACCTACAACCGCATCATCAACCAGATCTCTACCAACG  
AGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCACCCCTCTGCCCACTATGCCCACTCTC  
ACCAGCCTCCCATCTTCCACCGACAAGCCGTCGGGGCCATGGAGAGACTGCCTGCAGGCCCT  
GGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTCA  
TGCAGGTGTGGTTCGACACAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCCTG  
GATGGCTCTGTAACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGGTTTGGGAACATTGA  
CGGCGAATACTGGCTGGGCCTGGAGAACATTTACTGGCTGACGAACCAAGGCAACTACAAAC  
TCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTCTTTGCAGAATACGCCAGTTTCCGC  
CTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGCAATGCGGGTGA  
CTCCTTTACATGGCACAACGGCAAGCAGTTACACCACCTGGACAGAGATCATGATGTCTACA  
CAGGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAAC  
CTCAACGGGGTCTGGTACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTG  
GGCTGAGTTCCGAGGAGGCTCTTACTCACTCAAGAAAGTGGTGATGATGATCCGACCGAACC  
CCAACACCTTCCACT**TAA**AGCCAGCTCCCCCTCCTGACCTCTCGTGGCCATTGCCAGGAGCCCA  
CCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTTCATCCTGAGGCTGGGA  
GGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGAT  
ACGGTGTTTTCTGTCCCTCCTACTTTCTTACACACAGACAGCCCTCATGTCTCCAGGACA  
GGACAGGACTACAGACAACCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAAA

## FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA22779
><subunit 1 of 1, 493 aa, 1 stop
><MW: 57104, pI: 7.67, NX(S/T): 2
MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQ
QRVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLVEVDGGIVSEVKLLR
KESRNMNSRVTQLYMQLLHEIIRKRDNALELSQLENRIILNQTADMLQLASKYKDLEHKYQHL
ATLAHNQSEIIAQLEEHCQRVPSARPVPQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNL
KVLPPPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDGHDTSSIYLVKPEENTNRLMQVWCDQR
HDPGGWTVIQRRLDGSVNFERNWETYKQGGFNIDGEYWLGLENIYWLTNQGNKLLVTMEDW
SGRKVFAEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYHQ
KGGWWYNACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSYSLLKKVMMIRPNPNTFH
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-22

#### N-glycosylation sites.

amino acids 164-168, 192-196

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 124-128

#### Tyrosine kinase phosphorylation sites.

amino acids 177-184, 385-393, 385-394, 461-468

#### N-myristoylation sites.

amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347,  
465-471, 473-479

#### Amidation site.

amino acids 373-377

#### Fibrinogen beta and gamma chains C-terminal domain signature.

amino acids 438-451

#### Fibrinogen beta and gamma chains C-terminal domain proteins.

amino acids 305-343, 365-402, 411-424, 428-458

#### Trehalase proteins.

amino acids 275-292

CCCACGCGTCCGGCGCCCGTGGCCCTCGCGTCCATCTTTGGCCGTTCTCTCGGACCTGTCAAAA  
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
 GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT  
 GTTCCCTCTTTTCGGGGTCTCACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT  
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTTCAGTTGTTAAAAACAAATAGGATGCAAATTCC  
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAGAACTGAAAGTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
 CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
 GGCAGTAATACGGACTCTTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAA  
 TGATAAGATTTGATGTTTTTGGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

**FIGURE 5**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG  
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA  
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGGCGAAGTCGCGGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGGCAGCAAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
GTAGCCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCACCTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

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## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVFSSRVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEG YLYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMHNEST
```

### **N-glycosylation site.**

amino acids 242-246

### **Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

### **Tyrosine kinase phosphorylation site.**

amino acids 93-100

### **N-myristoylation site.**

amino acids 87-93, 231-237

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

### **HBGF/FGF family proteins**

amino acids 78-94, 102-153

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## **FIGURE 7**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGGAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

### FIGURE 8

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503
><subunit 1 of 1, 247 aa, 1 stop
><MW: 27702, pI: 10.36, NX(S/T): 2
MAAAIASGLIRQKRQAREQHWDRPSASRRRSSPSKNRGLCNGNLVDIFSKVRIFGLKKRRRLR
RQDPQLKGIIVTRL YCRQGY YLQMHPD GALDGT KDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
IAMNGEGYLYPSELTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKSKT
```

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198



## FIGURE 9

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCCTGGCA  
GACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCT  
GTGTCCAGACTGAGGCCCCATTTGCATTGTTTAACATACTTAGAAAATGAAGTGTTCAATTTT  
TAACATTCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGT  
GCTTGCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCCTCTCCA  
CGACTCGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGGCCGA  
CGTGCCCGAGCTCCTCCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCC  
TCGCGCGTCTTGGACATGCCAGGAATAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTG  
TCTTCCAAGCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGT  
CAGGACAGTGTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATG  
ATGTGTGTTAACCAAAATGGCGGGTATTTATGCATTCCCGGACAAACCCTGTGTATCGAGG  
GCCCTACTCGAACCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCAC  
TCTCAGTCCAAACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATG  
GATGAAAGCAACCAATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCC  
CACCCAGATCTGCATCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGC  
TTCTGGAAGGCCAGTGCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGT  
GCGAATGTTCTTGGATCCTATTCTTGTACATGCAACCCTGGTTTTTACCCTCAATGAGGATGG  
AAGGTCTTGCCAAGATGTGAACGAGTGTGCCACCGAGAACCCTGCGTGCAACCTGCGTCA  
ACACCTACGGCTCTCTCATCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTT  
CATTGCAGTGATATGGACGAGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAA  
CCAGCCCGGCACATACTTCTGCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAA  
GCTGCCAAGACATCAACGAATGTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGC  
TACAATTTACAAGGGGGCTTCAAATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAG  
GATCAGTGATAACCGCTGTATGTGTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTA  
CCATCTTGTACCGGGACATGGACGTGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAA  
ATGCAAGCCACGACCCGCTACCCTGGGGCTATTACATTTTCCAGATCAAATCTGGGAATGA  
GGGACAGAGAATTTTACATGCGGCAAACGGGGCCCCATCAGTGCCACCCTGGTGATGACACGCC  
CCATCAAAGGGCCCCGGGAAATCCAGCTGGACTTGGAATGATCACTGTCAACACTGTCATC  
AACTTCAGAGGCAGCTCCGTGATCCGACTGCGGATATATGTGTGCGCAGTACCCATTCTGAGC  
CTCGGGCTGGAGCCTCCGACGCTGCCTCTCATTGGCACCAAGGGACAGGAGAAGAGAGGAAA  
TAACAGAGAGAATGAGAGCGACACAGACGTTAGGCATTTCTTGCTGAACGTTTCCCCGAAGA  
GTCAGCCCCGACTTCCTGACTCTCACCTGTACTATTGCAGACCTGTACCCCTGCAGGACTTG  
CCACCCCCAGTTCCCTATGACACAGTTATCAAAAAGTATTATCATTGCTCCCCTGATAGAAGA  
TTGTTGGTGAATTTTCAAGGCCTTCAGTTTATTTCCACTATTTTCAAAGAAAATAGATTAGG  
TTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGTGAACAGCTTGCTGTCACTTCTTCACCTC  
TTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCAAAGACCCGGGAGCTGGCGGGGAACCTT  
GGGAGTAGCTAGTTTGTCTTTTTCGTACACAGAGAAGGCTATGTAAACAAACCACAGCAGGA  
TCGAAGGGTTTTTTAGAGAATGTGTTTCAAACCATGCCTGGTATTTTCAACCATAAAAGAAG  
TTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATCTGTCTTGTTCATTTTGAGTATTTTT  
AAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGACACATGCTATGTTCTGTCTTCCC  
AAACCCAGTCTCCTCTCCATTTTAGCCCAGTGTTTTCTTTGAGGACCCCTTAATCTTGCTTT  
CTTTAGAATTTTTACCCAATTGGATTGGAATGCAGAGGTCTCCAAACTGATTAAATATTTGA  
AGAGA

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## **FIGURE 10**

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQ  
NGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNO  
CVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLLEGQCLDIDECRYGYCQQLCANVPG  
SYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSILICRCDPGYELEEDGVHCSDM  
DECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQG  
GFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATT  
RYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGS  
SVIRLRIYVSQYPF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation sites.**

amino acids 283-287, 296-300

#### **N-myristoylation sites.**

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,  
267-273, 310-316

#### **Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

#### **Cell attachment sequence.**

amino acids 54-57

#### **Calcium-binding EGF-like.**

amino acids 131-166, 172-205, 211-245, 251-286

CAGGTTCCAACCTGCACCTTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGAACACAGGTCCTTGTTGCTGCAGAGAAGCAGTTGTTTTGCTG  
GAAGGAGGGAGTGC GCGGGCTGCCCCGGGCTCCTCCCTGCCGCCTCCTCTCAGTGGATGGTT  
CCAGGCACCTGTCTGGGGCAGGGAGGGCACAGGCCTGCACATCGAAGGTGGGGTGGGACCA  
GGCTGCCCTCGCCCCAGCATCCAAGTCCTCCCTTGGGCGCCCGTGGCCCTGCAGACTCTCA  
GGGCTAAGGTCCTCTGTTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGT  
AGCTTGAAGGAGGCACCA**ATG**CAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTG  
GCTCAGGCCTGCCCTGAGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTG  
TGCTACCGCGACCTAGAATCCGTGCCGCTGGCTTCCCGGCCAATGTGACTACACTGAGCC  
TGTCAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCAGGGAGGTGCCCTGCTGCAG  
TCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCTCTCTGAG  
CCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGC  
ACAACCTCAGTGCCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGC  
GACGCCTTCCGCAGCCTCCGTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGCACAC  
ATTGGCCGAGGGCACCCTTCACCCCGCTACCGCGCTGTCCCACCTGCAGATCAACGAGAACC  
CCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCCTGACCACGCGCCGTGTC  
ATCCCGGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGGTACACCGCTGAG  
CCGCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGG  
ATGGTGCCGAGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCG  
GCCCCCTCAGCTTCACTGGCACATCCAGATACCAGTGGCATTGTGGAGATCACCAGCCCCAA  
CGTGGGCACTGATGGGCGTGCCCTGCCTGGCACCCCTGTGGCCAGCTCCCAGCCGCGCTTCC  
AGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGGAGGAAGGCACCTAC  
AGCTGCCTGGCCACCAATGAGCTGGGCAGTGTCTGAGAGCTCAGTGGACGTGGCACTGGCCAC  
GCCCGGTGAGGGTGGTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGGTTGAGGGAA  
AGGGCTGCTATACGTTGACAACGAGGTGCAGCCATCAGGGCCGAGGACAATGTGGTTCATC  
ATCTACCTCAGCCGTGCTGGGAACCCTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCT  
GCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCCTTCTTCTTCTCCTC**ACCTCCTTCT**  
**AG**CCCCACCCAGGGCTTCCCTAACTCCTCCCTTGCCCCCTACCAATGCCCTTTAAGTGCTG  
CAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCT  
CCTTCTAATCTCTTCTAGAGCACCCTGCTATCCCCAACTTCTAGACCTGCTCCAAACTAGTGA  
CTAGGATAGAATTTGATCCCCTAACTCACTGTCTGCGGTGCTCATTTGCTGCTAACAGCATTG  
CCTGTGCTCTCCTCTCAGGGGCAGCATGCTAACGGGGCGACGTCCCTAATCCA**ACTGGGAGAA**  
GCCTCAGTGGTGGAATTCCAGGCACTGTGACTGTCAAGCTGGCAAGGGCCAGGATTTGGGGGA  
ATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGGAATGGGAGAGGAGGATGG  
GAAGTAGACAGTGGCTGGTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCT  
CCTTGCTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAA  
TGTGGGGATCCAGGATGGCCTTCTTCTTCTTACCCTTCTCCTCCTCAGCCTGCAACCTCTAT  
CCTGGAACCTGTCTCCTTCTTCTCCCCAACTATGCATCTGTTGTCTGCTCCTCTGCAAAGGC  
CAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTTCTGATGCCAAAAAAAAAAAAAAAAAA  
AAGGGCGGCCGCGACTCTAGAGTCGACCT

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## **FIGURE 12**

MQELHLLWWALLLGLAQACPEPCDCGEKYGFQIADCAYRDLESVPPGFPANVTTLSSLNRL  
PGLPEGAFREVPLLQSLWLAHNEIRTVAAGALASLSHLKSLDLSHNLISDFAWSDLHNL  
SALQLLKMSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINEN  
PFDCTCGIVWLKTWALTAVSIPEDQNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELR  
PGFVLALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANG  
SLLIPDFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHHGKAVEGKGCYTV  
DNEVQPSGPEDNVVVIYLSRAGNPEAAVAEGVPGQLPPGLLLLGQSLLLFFFLTSF

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **Transmembrane domain:**

amino acids 403-418

#### **N-glycosylation sites.**

amino acids 51-55, 120-124, 309-313

#### **Tyrosine kinase phosphorylation site.**

amino acids 319-326

#### **N-myristoylation sites.**

amino acids 14-20, 64-70, 92-98, 218-224, 294-300, 323-329,  
334-340, 350-356, 394-400

#### **Amidation site.**

amino acids 355-359

#### **Leucine rich repeats.**

amino acids 51-74, 75-98, 99-122, 123-146, 147-170

#### **Leucine rich repeat C-terminal domain.**

amino acids 180-230

CCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACAGCCCTGGCTGAGGGAGCTGC  
AGCGCAGCAGAGTATCTGACGGCGCCAGGTGCGTAGGTGCGGCACGAGGAGTTTTCCCGGC  
AGCGAGGAGGTCTTGAGCAGCATGGGCCGGAGGAGCGCCTTCCCTGCCGCCGCGCTCTGGCT  
CTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGCCGGGCCGCCGAGGAGGAGA  
GCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCATAGGATTTGAAGAAGATATC  
CTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGATTTCAGAAAAGCGCAACAGAG  
AATGCCAGCTATTCCTGTCAATATCCATTCCATGAATTTTACCTGGCAAGCTGCAGGGCAGG  
CAGAATACTTCTATGAATTCTGTCTTTCGCTCCCTGGATAAAGGCATCATGGCAGATCCA  
ACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCATCAGTTGTTCAAGTTGGTTT  
CCCATGTCTTGGAACACAGGATGGGGTGGCAGCATTTGAAGTGGATGTGATTGTTATGAATT  
CTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCTTCTTTAAACATGTCAACAA  
GCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAATGAAAGACGCATCTGCGAGTG  
TCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTGTACCCACGATGTATGAATG  
GTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTGGATTCTATGGAGTGAAGTGT  
GACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACCTGTTTCTACCCTGGAAAATG  
TATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAGCAAATGCCCACAACCCTGTC  
GAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTTCAAAGGTTACCAGGGAGAC  
CTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACATGGAACCTGCCATGAACCCAA  
CAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAATAAAAGGTACGAAGCCAGCC  
TCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGCACACGCCTTCACTTAAAAAG  
GCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGGTGAACTCCGACATCTGAAAC  
GTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTTCATGTGTTGAATGTTCAAATAA  
TGTTCAATTACACTTAAGAATACTGGCCTGAATTTTATTAGCTTCATTATAAATCACTGAGCT  
GATATTTACTCTTCCTTTTAAGTTTCTAAGTACGTCTGTAGCATGATGGTATAGATTTTCT  
TGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGATCAGGTAAAATTTTCAGTG  
TGTAAGTTGGCAGATATTTTCAAATTAACAATGCATTTATGGTGTCTGGGGGCAGGGGAACAT  
CAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAATTTGGATGGTGCAGTTAATGT  
TGAAGTTACAGCATTTTCAAGTTTTATTGTCAGATATTTAGATGTTTGTTACATTTTTTAAAAA  
TTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACCTTACCATTATTCCAGAGATT  
CAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATTTAAACAATATAATATATTCTA  
AACACAATGAAATAGGGAATATAATGTATGAACTTTTTGCATTGGCTTGAAGCAATATAATA  
TATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTATACTGTTTGTATGTATAAAAT  
AAAGGTGCTGCTTTTAGTTTTTTTGGAAAAA

## **FIGURE 14**

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal sequence.**

amino acids 1-28

**N-glycosylation sites.**

amino acids 88-92, 245-249

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

**FIGURE 15**

AGAACCTCAGAAATGTGAGTTATTTGGGAATGGCTGTTTGTAATGTCCTTACGTAAGCCAA  
GAGGAGGTCTTGACTTGGGGTCCCAGGGGTACCGCAGATCCCAGGGACTGGAGCAGCACTAG  
CAAGCTCTGGAGGATGAGCCAGGAGTCTGGAATTGAGGCTGAGCCAAAGACCCCAGGGCCGT  
CTCAGTCTCATAAAAGGGGATCAGGCAGGAGGAGTTTGGGAGAAACCTGAGAAGGGCCTGAT  
TTGCAGCATCATGATGGGCCTCTCCTTGGCCTCTGCTGTGCTCCTGGCCTCCCTCCTGAGTC  
TCCACCTTGGAAGTGGCACACGTGGGAGTGACATATCCAAGACCTGCTGCTTCCAATACAGC  
CACAAGCCCCTTCCCTGGACCTGGGTGCGAAGCTATGAATTCACCAGTAACAGCTGCTCCCA  
GCGGGCTGTGATATTCACTACCAAAGAGGCAAGAAAGTCTGTACCCATCCAAGGAAAAAAT  
GGGTGCAAAAATACATTTCTTTACTGAAAACCTCCGAAACAATTGTGACTCAGCTGAATTTTC  
ATCCGAGGACGCTTGGACCCCGCTCTTGGCTCTGCAGCCCTCTGGGGAGCCTGCGGAATCTT  
TTCTGAAGGCTACATGGACCCGCTGGGGAGGAGAGGGTGTTTCCTCCCAGAGTTACTTTAAT  
AAAGGTTGTTCATAGAGTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 16**

MMGLSLASAVLLASLLSLHLGTATRGSDISKTC CFQYSHKPLPWTWVRSYEFTSNSCSQRAV  
IFTTKRGKKVCTHPRKKWVQKYISLLKTPKQL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 3-9, 26-32

**Amidation site.**

amino acids 68-72

**Small cytokines (intecrine/chemokine).**

amino acids 23-88



## FIGURE 17

GCGAGAACCTTTGCACGCGCACAACTACGGGGACGATTTCTGATTGATTTTGGCGCTTTCGATCCACCCTCC  
 TCCCTTCTCATGGGGACTTTGGGGACAAAGCGTCCCGACCGCCTCGAGCGCTCGAGCAGGGCGCTATCCAGGAGC  
 CAGGACAGCGTCGGGAACAGACCATGGCTCCTGGACCCCAAGATCCTTAAGTTCGTCGCTTTCATCGTCGCGG  
 TTCTGCTGCCGGTCCGGGTTGACTCTGCCACCATCCCCGGCAGGACGAAGTTCGCCAGCAGACAGTGGCCCCA  
 CAGCAACAGAGGCGCAGCCTCAAGGAGGAGGAGTGTCCAGCAGGATCTCATAGATCAGAATATACTGGAGCCTG  
 TAACCCGTGCACAGAGGGTGTGGATTACACCATTGCTTCCAACAATTTGCCTTCTTGCCTGCTATGTACAGTTT  
 GTAAATCAGGTCAAACAAATAAAAGTTCCTGTACCACGACCAGAGACACCGTGTGTGAGTGTGAAAAAGGAAGC  
 TTCCAGGATAAAAACTCCCTGAGATGTGCCGGACGTGTAGAACAGGGGTGTCCAGAGGGGATGGTCAAGGTGAG  
 TAATTGTACGCCCCGGAGTGACATCAAGTGCAAAATGAATCAGCTGCCAGTTCCTGCGGAAAACCCAGCAG  
 CGGAGGAGACAGTGACCACCATCCTGGGGATGCTTGCCCTCTCCCTATCACTACCTTATCATCATAGTGGTTTTA  
 GTCATCATTTTAGCTGTGGTTGTGGTTGGCTTTTCATGTCCGAAGAAATTCATTTCTTACCTCAAAGGCATCTG  
 CTCAGGTGGTGGAGGAGGTCCCGAACGTGTGCACAGAGTCCCTTTCCGGCGGGCGTTTCATGTCCTTACAGTTT  
 CTGGGGCGGAGGACAATGCCCGCAACGAGACCGCTGAGTAACAGATACTTGACAGCCACCAAGGTCTCTGAGCAG  
 GAAATCCAAGGTGAGGAGCTGGCAGAGCTAACAGGTGTGACTGTAGAGTCGCCAGAGGAGCCACAGCGTCTGCT  
 GGAACAGGCAGAAGCTGAAGGGTGTGAGAGGAGGAGGCTGCTGGTTCCAGTGAATGACGCTGACTCCGCTGACA  
 TCAGCACCTTGCTGGATGCCTCGGCAACACTGGAAGAAGGACATGCAAGGAAACAATTCAGGACCAACTGGTG  
 GGCTCCGAAAAGCTCTTTTATGAAGAAGATGAGGCAGGCTCTGCTACGTCCTGCCTGTGAAAGAATCTCTTCAG  
 GAAACCAGAGCTTCCCTCATTTACCTTTTCTCCTACAAAGGGAAGCAGCCTGGAAGAAACAGTCCAGTACTTGA  
 CCCATGCCCCAACAACTCTACTATCCAATATGGGGCAGCTTACCAATGGTCTCTAGAACTTTGTTAACGCACCTT  
 GGAGTAATTTTTATGAAATACTGCGTGTGATAAGCAAACGGGAGAAATTTATATCAGATTCTTGGCTGCATAGT  
 TATACGATTGTGTATTAAGGGTCGTTTTAGGCCACATGCGGTGGCTCATGCCTGTAATCCCAGCAGCTTTGATAG  
 GCTGAGGCGAGTGGATTGCTTGAGCTCGGGAGTTTGAAGACAGCCTCATCAACACAGTGAAGTCCATCTCAAT  
 TTAAGAAAGAAAAAAGTGGTTTTAGGATGTGATCTTTCGAGTTCTTCATCATGAGACAAGTCTTTTTTCTGCTG  
 TTCTTATATTGCAAGCTCCATCTCTACTGGTGTGTGCATTTAATGACATCTAACTACAGATGCCGCACAGCCAC  
 AATGCTTTGCCTTATAGTTTTTTAACTTTAGAACGGGATTATCTTGTATTACCTGTATTTTCAGTTTCGGATA  
 TTTTTGACTTAATGATGAGATTATCAAGACGTAGCCCTATGCTAAGTCATGAGCATATGGAATTACGAGGGTTC  
 GACTTAGAGTTTTGAGCTTTAAGATAGGATTATTTGGGGCTTACCCCCACCTTAATTAGAGAAACATTTATATTG  
 CTTACTACTGTAGGCTGTACATCTCTTTCCGATTTTGTATAATGATGTAACATGGAAAACTTTAGGAAAT  
 GCACTTATTAGGCTGTTTACATGGGTTGCCTGGATACAAATCAGCAGTCAAAAATGACTAAAAATATACTAGT  
 GACGGAGGGAGAAATCCTCCCTCTGTGGGAGGCACTTACTGCATTCCAGTTCTCCCTCCTGCGCCCTGAGACTG  
 GACCAGGGTTTGATGGCTGGCAGCTTCTCAAGGGGCAGCTTGTCTTACTTGTAAATTTTAGAGGTATATAGCCA  
 TATTTATTTATAAATAAATATTTATTTATTTATTTATAAGTAGATGTTTACATATGCCAGGATTTTGAAGAGC  
 CTGGTATCTTTGGGAAGCCATGTGTCTGGTTTGTCTGCTGGGACAGTCATGGGACTGCATCTTCCGACTTGTG  
 CACAGCAGATGAGGACAGTGAGAATTAAGTTAGTCCGAGACTGCGAAGAGCTTCTCTTTCAAGCGCCATTACA  
 GTTGAACGTTAGTGAATCTTGAGCCTCATTTGGGCTCAGGGCAGAGCAGGTGTTTATCTGCCCCGGCATCTGCC  
 ATGGCATCAAGAGGGGAAGAGTGGACGGTGTCTGGGAATGGTGTGAAATGGTTGCCGACTCAGGCATGGATGGGC  
 CCTCTCGCTTCTGGTGGTCTGTGAACTGAGTCCCTGGGATGCCTTTTAGGGCAGAGATTCCTGAGCTGCGTTT  
 TAGGGTACAGATTCCCTGTTTGAGGAGCTTGCCCCCTCTGTAAGCATCTGACTCATCTCAGAGATATCAATTCT  
 TAAACACTGTGACAACGGGATCTAAATGGCTGACACATTTGTCTTGTGTACAGTTCCATATTTTTATTTAA  
 AACCTCAGTAATCGTTTTAGCTTCTTTCCAGCAAACCTCTTCTCCACAGTAGCCAGTCTGGTGGTAGGATAAATTA  
 CGGATATAGTCATTCTAGGGGTTTCAGTCTTTTCCATCTCAAGGCATTGTGTGTTTTGTTCCGGGACTGGTTTG  
 GCTGGGACAAAGTTAGAAGTGCCTGAAGTTCGCACATTAGATTGTTGTGTCCATGGAGTTTLAGGAGGGGATG  
 GCCTTTCCGGTCTTCGCACTTCCATCCTCTCCCACTTCCATCTGGCGTCCCACACCTTGTCCCCTGCACTTCTG  
 GATGACACAGGGTGTGCTGCCTCCTAGTCTTTGCCCTTTGTGGGCTTCTGTGCAGGAGACTTGGTCTCAAAG  
 CTCAGAGAGAGCCAGTCCGGTCCCAGCTCCTTTGTCCCTTCTCAGAGGCCTTCTTGAAGATGCATCTAGACT  
 ACCAGCCTTATCAGTGTTTAAGCTTATTCTTTAACATAAGCTTCTGACAACATGAAATGTTGGGGTTTTTT  
 GCGCTGGTTGATTTGTTTAGGTTTGTCTTATACCCGGGCCAAATAGCACATAACACCTGGTTATATATGAAA  
 TACTCATATGTTTATGACCAAAATAAATATGAAACCTCATRTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 18**

MGLWGQSVPTASSARAGRYPGARTASGTRPWLLDPKILKFVVFIVAVLLPVRVDSATIPRQD  
 EVPQQTVAPOQQRRSLKEEECPAGSHRSEYTGACNPCTEGVDYTIASNNLPSCLLCTVCKSG  
 QTNKSSCTTTTRDTVCQCEKGSFQDKNSPEMCRTCRTGCPGMVKVSNCTPRSDIKCKNESAA  
 SSTGKTPAAEETVTTILGMLASPHYLIIVVLVIILAVVVVVGFSRKKFISYLLKGICSGGG  
 GGPERVHRVLFRRRSCPSRVPGAEDNARNETLSNRYLQPTQVSEQEIQGQELAELTGVTVES  
 PEEPQRLLEQAEAEGCQRRRLLVPVNDADSADISTLLDASATLEEGHAKETIQDQVLVGSEKL  
 FYEDEAGSATSCL

**Important features of the protein:****Transmembrane domains:**

amino acids 35-52, 208-230

**N-glycosylation sites.**

amino acids 127-131, 182-186, 277-281

**Glycosaminoglycan attachment site.**

amino acids 245-249

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 260-264

**N-myristoylation sites.**

amino acids 21-27, 86-92, 102-108, 161-167, 242-248, 270-276,  
 297-303, 380-386

**ATP/GTP-binding site motif A (P-loop).**

amino acids 185-193

**TNFR/NGFR cysteine-rich region.**

amino acids 99-139

**FIGURE 19**

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCAGATGCACCCCT  
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACTGGGA  
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

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## **FIGURE 20**

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation sites.**

amino acids 120-124, 208-212

**Glycosaminoglycan attachment site.**

amino acids 80-84

**N-myristoylation sites.**

amino acids 81-87, 108-114, 119-125

**FIGURE 21**

CCGGGGAGGGGAGGGCCCGTCCCGCCCCCTCCCCGTCTCTCCCCGCCCCCTCCCCGTCCCTCCC  
GCCGAAGCTCCGTCCCGCCCCGCGGGCCGGCTCCGCCCTCACCTCCCGGCCGCGGGCTGCCCTC  
TGCCCGGGTTGTCCAAG**ATG**GAGGGCGCTCCACCGGGGTCGCTCGCCCTCCGGCTCCTGCTG  
TTCGTGGCGCTACCCGCCTCCGGCTGGCTGACGACGGGCGCCCCCGAGCCGCCGCCGCTGTC  
CGGAGCCCCACAGGACGGCATCAGAATTAATGTAACCTACACTGAAAGATGATGGGGACATAT  
CTAAACAGCAGGTTGTTCTTAACATAACCTATGAGAGTGGACAGGTGTATGTAAATGACTTA  
CCTGTAAATAGTGGTGTAAACCCGAATAAGCTGTCAGACTTTGATAGTGAAGAATGAAAATCT  
TGAAAATTTGGAGGAAAAAGAATATTTTGGAAATTGTCAGTGTAAAGGATTTTAGTTCATGAGT  
GGCCTATGACATCTGGTTCCAGTTTGCAACTAATTGTCATTCAAGAAGAGGTAGTAGAGATT  
GATGGAAAACAAGTTCAGCAAAGGATGTCAGTGAATTTGATATTTTAGTTAAGAACCGGGG  
AGTACTCAGACATTCAAACCTATACCCTCCCTTTGGAAGAAAGCATGCTCTACTCTATTTCTC  
GAGACAGTGACATTTTATTTACCCTTCCTAACCTCTCCAAAAAAGAAAGTGTAGTTCACTG  
CAAACCACTAGCCAGTATCTTATCAGGAATGTGGAAACCACTGTAGATGAAGATGTTTTACC  
TGGCAAGTTACCTGAAACTCCTCTCAGAGCAGAGCCGCCATCTTCATATAAGGTAATGTGTC  
AGTGGATGGAAAAGTTTAGAAAAGATCTGTGTAGGTTCTGGAGCAACGTTTTCCAGTATTC  
TTTCAGTTTTTTGAACATCATGGTGGTTGGAATTACAGGAGCAGCTGTGGTAATAACCATCTT  
AAAGGTGTTTTTCCCAGTTTCTGAATACAAAGGAATTCTTCAGTTGGATAAAGTGGACGTCA  
TACCTGTGACAGCTATCAACTTATATCCAGATGGTCCAGAGAAAAGAGCTGAAAACCTTGAA  
GATAAACATGTATT**TAA**ACGCCATCTCATATCATGGACTCCGAAGTAGCCTGTTGCCTCC  
AAATTTGCCACTTGAATATAATTTTCTTTAAATCGTT

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## **FIGURE 22**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60783
><subunit 1 of 1, 330 aa, 1 stop
><MW: 36840, pI: 4.84, NX(S/T): 4
MEGAPPGSLALRLLLFVALPASGWLTTGAPEPPPLSGAPQDGIRINVTTLKDDGDISKQQVV
LNITYESGQVYVNDLPVNSGVTRISCQTLIVKNENLENLEEKEYFGIVSVRILVHEWPMTSG
SSLQLIVIQEEVVEIDGKQVQKQDVTEIDILVKNRGVLRRHSNYTLPLEESMLYSISRDSIL
FTLPNLSKKESVSSLQTTTSQYLIRNVETTVDEDVLPGLPETPLRAEPPSSYKVMCQWMEKF
RKDLCRFWSNVFPVFFQFLNIMVVGITGAADVITILKVFFPVSEYKGILQLDKVDVIPVTAI
NLYPDGPPEKRAENLEDKTCI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 266-284

#### **Leucine zipper pattern.**

amino acids 155-176

#### **N-glycosylation sites.**

amino acids 46-49, 64-67, 166-169, 191-194

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## FIGURE 23

CGTCTCTGCGTTTCGCC**ATG**CGTCCCGGGGGCGCCAGGGCCACTCTGGCCTCTGCCCTGGGGGG  
 CCCTGGCTTGGGCCGTGGGCTTCGTGAGCTCCATGGGCTCGGGGAACCCCGCGCCCGGTGGT  
 GTTTGCTGGCTCCAGCAGGGCCAGGAGGCCACCTGCAGCCTGGTGCTCCAGACTGATGTCAC  
 CCGGGCCGAGTGCTGTGCCTCCGGCAACATTGACACCGCCTGGTCCAACCTCACCCACCCGG  
 GGAACAAGATCAACCTCCTCGGCTTCTTGGGCCTTGTCCTACTGCCTTCCCTGCAAAGATTCTG  
 TCGACGGCGTGAGTGCGGCCCGGGCAAGGCGTGCCGCATGCTGGGGGGCCGCCCGCGCTG  
 CGAGTGCGCGCCCGACTGCTCGGGGCTCCCGGCGCGGCTGCAGGTCTGCGGCTCAGACGGCG  
 CCACCTACCGCGACGAGTGCGAGCTGCGCGCCGCGCTGCCGCGGCCACCCGGACCTGAGC  
 GTCATGTACCGGGGCCGCTGCCGCAAGTCCCTGTGAGCACGTGGTGCTGCCCGCGGCCACAGTC  
 GTGCGTCTGTGGACCAGACGGGCAGCGCCACTGCGTGGTGTGTGAGCGGCGCCCTGCCCTG  
 TGCCCTCCAGCCCCGGCCAGGAGCTTTGCGGCAACAACAACGTACCTACATCTCCTCGTGC  
 CACATGCGCCAGGCCACCTGCTTCCCTGGGCGCTCCATCGGCGTGCGCCACGCGGGCAGCTG  
 CGCAGGCACCCCTGAGGAGCCGCCAGGTGGTGAGTCTGCAGAAGAGGAAGAGAAGTTCGTG**T**  
**GAG**CCTGCAGGACAGGCCTGGGCCTGGTGCCCGAGGCCCCCCATCATCCCTGTTATTTATT  
 GCCACAGCAGAGTCTAATTTATATGCCACGGACACTCCTTAGAGCCCGGATTCGGACCACTT  
 GGGGATCCCAGAACCTCCCTGACGATATCCTGGAAGGACTGAGGAAGGGAGGCCTGGGGGCC  
 GGCTGGTGGGTGGGATAGACCTGCGTTCCGGACACTGAGCGCCTGATTTAGGGCCCTTCTCT  
 AGGATGCCCCAGCCCCTACCCTAAGACCTATTGCCGGGGAGGATTCCACACTTCCGCTCCTT  
 TGGGGATAAACCTATTAATTATTGCTACTATCAAGAGGGCTGGGCATTCTCTGCTGGTAATT  
 CCTGAAGAGGCATGACTGCTTTTCTCAGCCCCAAGCCTCTAGTCTGGGTGTGTACGGAGGGT  
 CTAGCCTGGGTGTGTACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGAG  
 TACGGAGGGTCTAGCCTGGGTGAGTACGGAGGGTCTAGCCTGGGTGTGTATGGAGGATCTAG  
 CCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATG  
 GAGGGTCTAGCCTGGGTGAGTATGGAGGGTCTAGCCTGGGTGTGTATGGAGGGTCTAGCCTG  
 GGTGAGTATGGAGGGTCTAGCCTGGGTGTGTACGGAGGGTCTAGTCTGAGTGCCTGTGGGGA  
 CCTCAGAACACTGTGACCTTAGCCCAGCAAGCCAGGCCCTTCATGAAGGCCAAGAAGGCTGC  
 CACCATTCCCTGCCAGCCCCAAGAACTCCAGCTTCCCCACTGCCTCTGTGTGCCCTTTGCGT  
 CCTGTGAAGGCCATTGAGAAATGCCAGTGTGCCCCCTGGGAAAGGGCACGGCCTGTGCTCC  
 TGACACGGGCTGTGCTTGGCCACAGAACCACCCAGCGTCTCCCCTGCTGCTGTCCACGTCAG  
 TTCATGAGGCAACGTCGCGTGGTCTCAGACGTGGAGCAGCCAGCGGCAGCTCAGAGCAGGGC  
 ACTGTGTCCGGCGGAGCCAAGTCCACTCTGGGGGAGCTCTGGCGGGGACCACGGGCCACTGC  
 TCACCCACTGGCCCCGAGGGGGGTGTAGACGCCAAGACTCACGCATGTGTGACATCCGGAGT  
 CCTGGAGCCGGGTGTCCCAGTGGCACCACTAGGTGCCTGCTGCCTCCACAGTGGGGTTTACA  
 CCCAGGGCTCCTTGGTCCCCACAACCTGCCCCGGCCAGGCCTGCAGACCCAGACTCCAGCC  
 AGACCTGCCTCACCCACCAATGCAGCCGGGGCTGGCGACACCAGCCAGGTGCTGGTCTTGGG  
 CCAGTTCTCCACGACGGCTCACCCCTCCCTCCATCTGCGTTGATGCTCAGAATCGCCTACC  
 TGTGCCTGCGTGTAAACCACAGCCTCAGACCAGCTATGGGGAGAGGACAACACGGAGGATAT  
 CCAGCTTCCCCGGTCTGGGGTGAGGAATGTGGGGAGCTTGGGCATCCTCCTCCAGCCTCCTC  
 CAGCCCCCAGGCAGTGCCCTTACCTGTGGTGCCAGAAAAGTGCCCCCTAGGTTGGTGGGTCTA  
 CAGGAGCCTCAGCCAGGCAGCCACCCACCCCTGGGGCCCTGCCTCACCAAGGAAATAAAGA  
 CTAAGCCATAAAAAAA

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## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62306

<subunit 1 of 1, 263 aa, 1 stop

<MW: 27663, pI: 6.77, NX(S/T): 2

MRPGAPGPLWPLPWGALAWAVGFVSSMSGGNPAPGGVCWLQQGQEATCSLVLQTDVTRA ECC  
ASGNIDTAWSNLTHPGNKINLLGFLGLVHCLPCKDSCDGV ECGPGKACRMLGGRPRCECAPD  
CSGLPARLQVCGSDGATYRDECELRAARCRGHPDLSVMYRGRCRKSC EHVVCPRPQSCVVDQ  
TGAHCVVCRAAPCPVPSSPGQELCGNNNVTYISSCHMRQATCFLGRSIGVRHAGSCAGTPE  
EPPGGESAEEEEENFV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation sites.**

amino acids 73-77, 215-219

#### **Osteonectin domain proteins.**

amino acids 97-130, 169-202



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## FIGURE 25

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGT  
TGTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGAT  
AAAATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAA  
ATTTGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCCCGCTGGCTA  
CCATGATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTTCATCCATCCTTTAAATCTG  
CACATGAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACT  
GGGGATATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGA  
TTAAATTAGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTG  
TTAGACAAGTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTCGA  
AAAATTACTTCATGCTCTAGGAGGAGATGACTTCCTTGGGAATGCTTAATCGAACACTTCTTG  
AAACCTTGCAAAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATG  
AGGGTCAATTATGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCCTG  
TTCTGATTCTGGCCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGC  
AGGCATCCAAAAGCAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACC  
AAGTACACAGGAAATCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAACAGAGACTCG  
TTCAGACTTCTATGACATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGCAATATTA  
CTTTTCTCAACTTTGATCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACA  
ACTTTAGTTAAGGGGGAATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGG  
CCTTAATACAGTTTTTAACCACTGATAATTGAGATTTGTTTCATTAAACAGTATTGGGATTGTGC  
CCTCTGTGAGAGAAAAGGAAGATCCTGAGCCATCAACAGATGGAACATATGTTTGGGAAGATC  
TTTTCCCAAGAACTCTTACTAAAGCACAAATTTTAAAGCTCTTCTGTCCTATGATTATGC  
TGTGAAGAAGCCATGGCTTGCAATATCCTCACTATAAGCCCCCGGAGAAATGCCCTCTATCA  
TTCTCCATGATCGACTTTATTACCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATG  
AGTGCCATTGCAGCCCACAACGCTGCACTCCTTGCCATATCACCGCTGGAACGGGCACACAGA  
CATGATTGATCAGGATGGCTTATATGAGAACTTAAAACTGAACTAT**TGA**AGTGACACACTCC  
TTTTTCCCCTCCTAGTTCCAAATGACTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGA  
TGATTTTGAACCAGATATTTTGCCATTATCATTGTTTAATAAAAGTAATCCCTGCTGGTCAT  
AGGAAAAAAAAAAAAA

## **FIGURE 26**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880

<subunit 1 of 1, 505 aa, 1 stop

<MW: 56640, pI: 6.10, NX(S/T): 4

MGRVVAELVSSLLGLWLLLCSCGCPEGAE LRAPPDKIAIIGAGIGGTS AAYYLRQKFGKDVK  
IDLFEREEVGGRLATMMVQGGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGE  
TLVFEE SNWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHAL  
GGDDFLGMLNRTLLET LQKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLW  
AVEGGNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDI  
VLVATPLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT  
TDNSDLFINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWL  
AYPHYKPPKECPSIILHDLRYLLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDG  
LYEKLKTEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation sites.**

amino acids 196-200, 323-327, 353-357

#### **Tyrosine kinase phosphorylation site.**

amino acids 291-298

#### **N-myristoylation sites.**

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,  
119-125, 260-266, 384-390, 459-465

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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## **FIGURE 27**

CATTTCCAACAAGAGCACTGGCCAAGTCAGCTTCTTCTGAGAGAGTCTCTAGAAGAC**ATGAT**  
GCTACACTCAGCTTTGGGTCTCTGCCTCTTACTCGTCACAGTTTCTTCCAACCTTGCCATTG  
CAATAAAAAAGGAAAAGAGGCCTCCTCAGACACTCTCAAGAGGATGGGGAGATGACATCACT  
TGGGTACAACTTATGAAGAAGGTCTCTTTTATGCTCAAAAAAGTAAGAAGCCATTAATGGT  
TATTCATCACCTGGAGGATTGTCAATACTCTCAAGCACTAAAGAAAGTATTTGCCCAAATG  
AAGAAATACAAGAAATGGCTCAGAATAAGTTCATCATGCTAAACCTTATGCATGAAACCACT  
GATAAGAATTTATCACCTGATGGGCAATATGTGCCTAGAATCATGTTTGTAGACCCCTTCTTT  
AACAGTTAGAGCTGACATAGCTGGAAGATACTCTAACAGATTGTACACATATGAGCCTCGGG  
ATTTACCCCTATTGATAGAAAACATGAAGAAAGCATTAAAGACTTATTCAGTCAGAGCTA**TAA**  
GAGATGATGGAAAAAAGCCTTCACTTCAAAGAAGTCAAATTTTCATGAAGAAAACCTCTGGCA  
CATTGACAAATACTAAATGTGCAAGTATATAGATTTTGTAATATTACTATTTAGTTTTTTTA  
ATGTGTTTGCAATAGTCTTATTAAAATAAATGTTTTTTAAATCTGA

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## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64896

<subunit 1 of 1, 166 aa, 1 stop

<MW: 19171, pI: 8.26, NX(S/T): 1

MMLHSALGLCLLLVTVSSNLAIKKEKRPPQTLSRGWGDDITWVQTYEEGLFYAQKSKKPL  
MVIHHLEDCQYSQALKKVFAQNEEIQEMAQNKFIMLNLMHETTDKNLSPDGQYVPRIMFVDP  
SLTVRADIAGRYSNRLYTYEPRDLPLLIENMKKALRLIQSEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-myristoylation site.**

amino acids 51-57

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## **FIGURE 29**

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGA  
AAGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCA  
GTGGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAG  
CGATGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTTCGCCCACTTCCAC  
CAATTCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCT  
GCCCCTACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGG  
TCACCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAA  
AACAAATGTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTA  
ATAAACATGAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9700, pI: 9.55, NX(S/T): 0

MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFP  
WFRRNFPIPIPIESAPTTPLPSEK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Homologous region to B3-hordein:**

amino acids 47-85

## FIGURE 31

CGGACGCGTGGGCGGGCGCGCCGGGAGGGACCGGCGGCGGC**ATGGG**CGGGGGCCCTGGGAT  
GCGGGCCCGTCTCGCCGCTGCTGCCGCTGTTGCTGCTGCTCGGCCTGGCCCGGGCGCCGC  
GGGAGCGCCGGGCCCCGACGGTTTAGACGTCTGTGCCACTTGCCATGAACATGCCACATGCC  
AGCAAAGAGAAGGGAAGAAGATCTGTATTTGCAACTATGGATTTGTAGGGAACGGGAGGACT  
CAGTGTGTTGATAAAAATGAGTGCCAGTTTGGAGCCACTCTTGTCTGTGGGAACACACATC  
TTGCCACAACACCCCCGGGGGCTTCTATTGCATTTGCCTGGAAGGATATCGAGCCACAAACA  
ACAACAAGACATTTCATTCCCAACGATGGCACCTTTTGTACAGACATAGATGAGTGTGAAGTT  
TCTGGCCTGTGCAGGCATGGAGGGCGATGCGTGAACACTCATGGGAGCTTTGAATGCTACTG  
TATGGATGGATACTTGCCAAGGAATGGACCTGAACCTTTCCACCCGACCACCGATGCCACAT  
CATGCACAGAAATAGACTGTGGTACCCCTCCTGAGGTTCCAGATGGCTATATCATAGGAAAT  
TATACGTCTAGTCTGGGCAGCCAGGTTGCTTATGCTTGCAGAGAAGGATTTCTCAGTGTTC  
AGAAGATACAGTTTCAAGCTGCACAGGCCTGGGCACATGGGAGTCCCCAAAATTACATTGCC  
AAGAGATCAACTGTGGCAACCCTCCAGAAATGCGGCACGCCATCTTGCTAGGAAATCACAGC  
TCCAGGCTGGGCGGTGTGGCTCGCTATGTCTGTCAAGAGGGCTTTGAGAGCCCTGGAGGAAA  
GATCACTTCTGTTTGCACAGAGAAAGGCACCTGGAGAGAAAGTACTTTAACATGCACAGAAA  
TTCTGACAAAGATTAATGATGTATCACTGTTTAAATGATACCTGTGTGAGATGGCAAATAAAC  
TCAAGAAGAATAAAACCCCAAGATCTCATATGTGATATCCATAAAAAGGACAACGGTTGGACCC  
TATGGAATCAGTTTCGTGAGGAGACAGTCAACTTGACCACAGACAGCAGGACCCAGAAAGTGT  
GCCTAGCCCTGTACCCAGGCACCAACTACACCGTGAACATCTCCACAGCACCTCCCAGGCGC  
TCGATGCCAGCCGTCATCGGTTTCCAGACAGCTGAAGTTGATCTCTTAGAAGATGATGGAAG  
TTTCAATATTTCAATATTTAATGAACTTGTGTTGAAATTGAACAGGCGTTCTAGGAAAGTTG  
GATCAGAACACATGTACCAATTTACCGTTCTGGGTGAGAGGTGGTATCTGGCTAACTTTTCT  
CATGCAACATCGTTTAACTTCACAACGAGGGAACAAGTGCCTGTAGTGTGTTTGGATCTGTA  
CCCTACGACTGATTATACGGTGAATGTGACCCTGCTGAGATCTCCTAAGCGGCACTCAGTGC  
AAATAACAATAGCAACTCCCCCAGCAGTAAACAGACCATCAGTAACATTTTCAGGATTTAAT  
GAAACCTGCTTGAGATGGAGAAGCATCAAGACAGCTGATATGGAGGAGATGTATTTATTCCA  
CATTTGGGGCCAGAGATGGTATCAGAAGGAATTTGCCCAGGAAATGACCTTTAATATCAGTA  
GCAGCAGCCGAGATCCCGAGGTGTGCTTGGACCTACGTCCGGGTACCAACTACAATGTCAGT  
CTCCGGGCTCTGTCTTCGGAACCTTCTGTGGTCACTCTCCCTGACAACCCAGATAACAGAGCC  
TCCCCTCCCGGAAGTAGAATTTTTTACGGTGCACAGAGGACCTCTACCACGCCTCAGACTGA  
GGAAAGCCAAGGAGAAAAATGGACCAATCAGTTCATATCAGGTGTTAGTGCTTCCCCTGGCC  
CTCCAAAGCACATTTTCTTGTGATTCTGAAGGCGCTTCCCTCCTTCTTTAGCAACGCCTCTGA  
TGCTGATGGATACGTGGCTGCAGAACTACTGGCCAAAGATGTTCCAGATGATGCCATGGAGA  
TACCTATAGGAGACAGGCTGTACTATGGGGAATATTATAATGCACCCTTGAAAAGAGGGAGT  
GATTACTGCATTATATTACGAATCACAAAGTGAATGGAATAAGGTGAGAAGACACTCCTGTGC  
AGTTTGGGCTCAGGTGAAAGATTCGTCACTCATGCTGCTGCAGATGGCGGGTGTTGGACTGG  
GTTCCCTGGCTGTTGTGATCATTCTCACATTCCCTCTCCTTCTCAGCGGTG**TGA**TGGCAGATG  
GACACTGAGTGGGGAGGATGCACTGCTGCTGGGCAGGTGTTCTGGCAGCTTCTCAGGTGCC  
GCACAGAGGCTCCGTGTGACTTCCGTCCAAGGAGCATGTGGGCCTGCAACTTTCTCCATTCC  
CAGCTGGGCCCCATTCTGGATTTAAGATGGTGGCTATCCCTGAGGAGTCACCATAAGGAGA  
AACTCAGGAATTCTGAGTCTTCCCTGCTACAGGACCAGTTCTGTGCAATGAACTTGAGACT  
CCTGATGTACACTGTGATATTGACCGAAGGCTACATACAGATCTGTGAATCTTGGCTGGGAC  
TTCTCTGAGTGTGCTGAGGGTCACTCCTCTAGACATTGACTGCAAGAGAATCTCTGCA  
ACCTCCTATATAAAAGCATTTCTGTTAATTCATTGCAATCCATTCTTTACAATATGCAGTG  
AGATGGGCTTAAGTTTGGGCTAGAGTTTGACTTTATGAAGGAGGTGATTGAAAAAGAGAAC  
GTGACGTAGGCAAATGTTTCAAGCACTTTAGAAACAGTACTTTTCCTATAATTAGTTGATAT  
ACTAATGAGAAAATATACTAGCCTGGCCATGCCAATAAGTTTCCCTGCTGTGTCTGTTAGGCA  
GCATTGCTTTGATGCAATTTCTATTGTCCTATATATTCAAAGTAATGTCTACATTCCAGTA  
AAAATATCCCGTAATTAAAAA

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## FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96031
><subunit 1 of 1, 747 aa, 1 stop
><MW: 82710, pI: 6.36, NX(S/T): 18
MGRGPWDAGPSRRLPLLLLLGLARGAAGAPGPDGLDVCATCHEHATCQOREGKKICICNYG
FVGNGRTQCVDKNECQFGATLVCGNHTSCHNTPGGFYCICLEGYRATNNNKTFIPNDGTFCT
DIDECEVSGLCRHGGRCVNTHGSEFCYCMDGYLPRNGPEPFHPTTDATEIDCGTPPEVP
DGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTWESPKLHCQEINCGNPPEMRHA
ILVGNHSSRLGGVARYVCQEGFESPGGKITSVCTEKGWTRESTLTCTEILTINLVSLFNDT
CVRWQINSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVCLALYPGTNYTVNI
STAPPRRSMFAVIGFQTAEVDLLEDDGSFNISIFNETCLKLNRRSRKVGSEHMYQFTVLGQR
WYLANFSHATSFNFTTREQVPVVCCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPAVKQTI
SNISGFNETCLRWRSIKTADMEEMYLFIHWGQRWYQKEFAQEMTFNIISSSSRDPEVCLDLRP
GTNYNVSLRALSSELPPVISLTQTITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQ
VLVLPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAQDVPDDAMEIPIGDRLYYGEYYN
APLKRGSYCIILRITSEWNKVRHSCAVWAQVKDSSLMLLQMAVGLGSLAVVILTFLSF
SAV
```

### Important features of the protein:

#### Signal peptide:

amino acids 1-29

#### Transmembrane domain:

amino acids 718-740

#### N-glycosylation sites.

amino acids 87-91, 112-116, 193-197, 253-257, 308-312, 348-352, 367-371, 371-375, 402-406, 407-411, 439-443, 447-451, 470-474, 498-502, 503-507, 542-546, 563-567, 645-649

#### cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 478-482, 686-690, 705-709

#### Tyrosine kinase phosphorylation site.

amino acids 419-427

#### N-myristoylation sites.

amino acids 22-28, 35-41, 65-71, 86-92, 96-102, 120-126, 146-152, 192-198, 252-258, 274-280, 365-371, 559-565, 688-694, 727-733.

#### Amidation site.

amino acids 52-56

#### Aspartic acid and asparagine hydroxylation sites.

amino acids 91-103, 141-153.

#### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 624-635

#### Cytochrome c family heme-binding site signature.

amino acids 39-45

#### Calcium-binding EGF-like domain proteins pattern proteins.

amino acids 85-106, 135-156

#### Receptor tyrosine kinase class V proteins:

amino acids 389-422



## FIGURE 33

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
TGCCCGCTATGACTCTAGCACCCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA  
GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAAACATCTCCCAACTTCATGGTGC  
TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCTTTGCACCGA  
TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
CAGAAGCTAAGGGCCTGTCCTCAGAGAGCAGTGCCCTCTTCCGACGGCCCCCATCCAGTCATC  
ACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCC  
GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAT  
GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTCCAGCATCCCTGGGGCCTCAGA  
CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTCACAGCCTCTGCCGAGACCCTGTCC  
ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA  
CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC  
CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGGCCCTTCCCCACCAGCAGGGACCCT  
CTTCCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC  
GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG  
TGGCTTCCCCGGAAGACCTCACTGACCCACAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
CGGGAACCTCACGCCCACGCGCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTTAGCCTG  
GGCCCCCACCAGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
AAGGGCAGCATGTCCAAGCCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC  
CGGAGTGTATGTATGGGGAGGGGCTTCACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG  
CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
TTAAAATTCACTCAGTGTGGCCCCAAAAAAA

**FIGURE 34**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108722
><subunit 1 of 1, 482 aa, 1 stop
><MW: 49060, pI: 4.74, NX(S/T): 4
MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTLSEA
ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSPNFMVLIATSVETSAASGSPEGAGM
TTVQTITGSDPEEAIFDTLCTDDSSSEEAKTLTMDILTTLAHTSTEAKGLSSESSASSDGPHPV
ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLLEALVTVTNI
EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY
VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPSTRD
PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 252-256, 445-449, 451-455

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-88

**N-myristoylation sites.**amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284,  
314-320, 349-355, 386-392, 397-403, 449-455**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

**FIGURE 35**

GCCTCTGAATTGTTGGGCAGTCTGGCAGTGGAGCTCTCCCCGGTCTGACAGCCACTCCAGAG  
GCC**ATG**CTTCGTTTCTTGCCAGATTTGGCTTTCAGCTTCCTGTTAATTCTGGCTTTGGGCCA  
GGCAGTCCAATTTCAAGAATATGTCTTTCTCCAATTTCTGGGCTTAGATAAGGCGCCTTCAC  
CCCAGAAGTTCCAACCTGTGCCTTATATCTTGAAGAAAATTTTCCAGGATCGCGAGGCAGCA  
GCGACCACTGGGGTCTCCCGAGACTTATGCTACGTAAAGGAGCTGGGCGTCCGCGGGAATGT  
ACTTCGCTTTCTCCCAGACCAAGGTTTCTTTCTTTACCCAAAGAAAATTTCCCAAGCTTCCT  
CCTGCCTGCAGAAGCTCCTCTACTTTAACCTGTCTGCCATCAAAGAAAGGGAACAGTTGACA  
TTGGCCCAGCTGGGCCTGGACTTGGGGCCCAATTCTTACTATAACCTGGGACCAGAGCTGGA  
ACTGGCTCTGTTCTGTTTCAGGAGCCTCATGTGTGGGGCCAGACCACCCCTAAGCCAGGTA  
AAATGTTTGTGTTGCGGTCAGTCCCATGGCCACAAGGTGCTGTTCACTTCAACCTGCTGGAT  
GTAGCTAAGGATTGGAATGACAACCCCCGGAAAAATTTCTGGGTTATTCCTGGAGATACTGGT  
CAAAGAAGATAGAGACTCAGGGGTGAATTTTCAGCCTGAAGACACCTGTGCCAGACTAAGAT  
GCTCCCTTCATGCTTCCCTGCTGGTGGTGA CTCTCAACCCTGATCAGTGCCACCCTTCTCGG  
AAAAGGAGAGCAGCCATCCCTGTCCCCAAGCTTTCTTGTAAGAACCTCTGCCACCGTCACCA  
GCTATTCATTA ACTTCCGGGACCTGGGTGGCACAAGTGGATCATTGCCCCCAAGGGGTTC A  
TGGCAAATTACTGCCATGGAGAGTGTCCCTTCTCACTGACCATCTCTCTCAACAGCTCCAAT  
TATGCTTTCATGCAAGCCCTGATGCATGCCGTTGACCCAGAGATCCCCCAGGCTGTGTGTAT  
CCCCACCAAGCTGTCTCCCATTTCCATGCTCTACCAGGACAATAATGACAATGTCATTCTAC  
GACATTATGAAGACATGGTAGTCGATGAATGTGGGTGTGGG**TAG**GATGTCAGAAATGGGAAT  
AGAAGGAGTGTTCCTTAGGGTAAATCTTTTAATAAAACTACCTATCTGGTTTATGACCACTTA  
GATCGAAATGTC

**FIGURE 36**

MLRFLPDLAFSFLLILALGQAVQFQEYVFLQFLGLDKAPSPQKFQVPYILKKIFQDREAAA  
TTGVSRDLCYVKELGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTL  
AQLGLDLGPNSYYNLGPELELALFLVQEPHVWGQTPKPGKMFVLRSPWPQGAVHFNLLDV  
AKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLLVVTLNPDQCHPSRK  
RRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYPCHGECPFSLTISLNSSNY  
AFMQALMHAVDPEIPQAVCIPTKLSPISMPLYQDNNDNVILRHYEDMVVDECGCG

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 112-116, 306-310

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 96-100

**N-myristoylation site.**

amino acids 77-83

**TGF-beta family proteins.**

amino acids 264-299, 327-341, 345-364

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## FIGURE 37

CAC TTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC  
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA  
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTTCCCCTGCTCTGTT  
TCCTTCACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA  
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGGACGGAGGGCCCCGGCAGGAAG**ATG**GGC  
TCCCGTGGACAGGGACTCTTGCTGGCGTACTGCCTGCTCCTTGCCTTTGCCTCTGGCCTGGT  
CCTGAGTCGTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC  
CGTCGCCTCCGGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCAGTCAG  
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC  
GGCGACCGCCGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGACCGCGGAG  
ATCGAGGCTCCAAGGGAAATATGGCAAACAGGCTCAGCAGGGGGCCAGGGGCCACACTGGA  
CCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC  
CTTTTCGGTGGGCGGAAGAAGCCATGCACAGCAACCACTACTACCAGACGGTACTCTTCG  
ACACGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCGGCAAGTTCTACTGCTAC  
GTGCCCCGCCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT  
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTTCGCGCAGGTGGGCGACCGCAGCA  
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC  
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG  
TGGCTACCTGGTCAAGCACGCCACCGAGCCC**TAG**CTGGCCGGCCACCTCCTTTCTCTCGCC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC  
CCTGGCTTTGGCATTCAAGTGAAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGGCACCCGC  
GAGAACCCTCTGGGACCTTCCGCGGCCCTCTCTGCACACATCCTCAAGTGACCCCGCACGGC  
GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGGCTCCAGTCTTGGAATA  
ATTAGGCAAATTCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
TTGTTATTTTTGTCTTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCCTTTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATTCTTTTAAGCCACGTAGGAACCTTTCTTGAGGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT  
GATGGGGGCTGGGGCCCCAGGCGTCAGCCTCCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC  
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCCTGACAGTGCCAGGGACCCCTGGGTCCCCCA  
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCTGGCATCGGCT  
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCCGGGGCCTTGGCTTCTGTTTTT  
TATAAAACACCTCAAGCAGCACTGCAGTCTCCATCTCCTCGTGGGCTAAGCATCACCGCTT  
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCCCT  
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG  
CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCAGTCTCAGGAGC  
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG  
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCC  
ATAGCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC  
CCCAAACCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTTGACTAATCCTGC  
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
CTGCGGGTCAAGTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC  
GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP
```

**Signal sequence.**

amino acids 1-25

**N-glycosylation site.**

amino acids 93-97

**N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

**Amidation site.**

amino acids 150-154

**Cell attachment sequence.**

amino acids 104-107

**FIGURE 39**

GAATTCGGCACGAGGGAAGAAGAGAAAGAAAATCTCCGGGGCTGCTGGGAGCATATAAAGAA  
GCCCTGTGGCCTTGCTGGTTTTACCATCCAGACCAGAGTCAGGCCACAGACGGAC**ATG**GCTG  
CTCAAGGCTGGTCCATGCTCCTGCTGGCTGTCCTTAACCTAGGCATCTTCGTCCGTCCCTGT  
GACACTCAAGAGCTACGATGTCTGTGTATTCAGGAACACTCTGAATTCATTCCTCTCAAAC  
CATTA AAAATATAATGGTGATATTCGAGACCATTTACTGCAACAGAAAGGAAGTGATAGCAG  
TCCCCAAAAATGGGAGTATGATTTGTTTGGATCCTGATGCTCCATGGGTGAAGGCTACTGTT  
GGCCAATTACTAACAGGTTCCCTACCTGAGGACCTCAAACAAAAGGAATTTCCACCGGCAAT  
GAAGCTTCTGTATAGTGTTGAGCATGAAAAGCCTCTATATCTTTTCATTTGGGAGACCTGAGA  
ACAAGAGAATATTTCCCTTTCCAATTCGGGAGACCTCTAGACACTTTGCTGATTTAGCTCAC  
AACAGTGATAGGAATTTTCTACGGGACTCCAGTGAAGTCAGCTTGACAGGCAGTGATGCC**TA**  
**AA**AGCCACTCATGAGGCAAAGAGTTTCAAGGAAGCTCTCCTCCTGGAGTTTTGGCGTTCTCA  
TTCTTATACTCTATTCCCGCGTTAGTCTGGTGTATGGATCTATGAGCTCTCTTTTAATATTT  
TATTATAAATGTTTTATTTACTTAACTTCCTAGTGAATGTTACAGGTGACTGCTCCCCCAT  
CCCCATTTCTTGATATTACATATAATGGCATCATATAACCCCTTTATTGACTGACAAACTACT  
CAGATTGCTTAACATTTTGTGCTTCAAAGTCTTATCCCACTCCACTATGGGCTGTTACAGAG  
TGCATCTCGGTGTAGAGCAAGGCTCCTTGTCTTCAGTGCCCCAGGGTGAAATACTTCTTTGA  
AAAATTTTCATTCATCAGAAAATCTGAAATAAAAATATGTCTTAATTGAG

40/75

## **FIGURE 40**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73838
><subunit 1 of 1, 167 aa, 1 stop
><MW: 19091, pI: 7.48, NX(S/T): 1
MAAQGWSMLLLAVLNLGIFVRPCDTQELRCLCIQEHSEFIPLKLIK NIMVIFETIYCNRKEV
IAVPKNGSMICLDPDAPWVKATVGPITNRFLPEDLKQKEFPPAMKLLYSVEHEKPLYLSFGR
PENKRIFPFPIRETSRHFADLAHNSDRNFLRDSSEVSLTGSDA
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-25

#### **N-glycosylation site.**

amino acids 68-72

#### **N-myristoylation site.**

amino acids 69-75

#### **Small cytokines (intercrine/chemokine) C-x-C subfamily signature**

amino acids 40-85



41/75

## **FIGURE 41**

CAGAC**ATG**GCTCAGTCACTGGCTCTGAGCCTCCTTATCCTGGTTCTGGCCTTTGGCATCCCC  
 AGGACCCAAGGCAGTGATGGAGGGGCTCAGGACTGTTGCCTCAAGTACAGCCAAAGGAAGAT  
 TCCCGCCAAGGTTGTCCGCAGCTACCGGAAGCAGGAACCAAGCTTAGGCTGCTCCATCCCAG  
 CTATCCTGTTCTTGCCCCGCAAGCGCTCTCAGGCAGAGCTATGTGCAGACCCAAAGGAGCTC  
 TGGGTGCAGCAGCTGATGCAGCATCTGGACAAGACACCATCCCCACAGAAACCAGCCCAGGG  
 CTGCAGGAAGGACAGGGGGGCCTCCAAGACTGGCAAGAAAGGAAAGGGCTCCAAGGCTGCA  
 AGAGGACTGAGCGGTCACAGACCCCTAAAGGGCCA**TAG**CCCAGTGAGCAGCCTGGAGCCCTG  
 GAGACCCCAACAGCCTCACCAGCGCTTGAAGCCTGAACCCAAGATGCAAGAAGGAGGCTATG  
 CTCAGGGGGCCCTGGAGCAGCCACCCCATGCTGGCCTTGCCACACTCTTTCTCCTGCTTTAAC  
 CACCCCATCTGCATTCCCAGCTCTACCCTGCATGGCTGAGCTGCCCACAGCAGGCCAGGTCC  
 AGAGAGACCGAGGAGGGAGAGTCTCCCAGGGAGCATGAGAGGAGGCAGCAGGACTGTCCCT  
 TGAAGGAGAATCATCAGGACCCTGGACCTGATACGGCTCCCCAGTACACCCACCTCTTCCT  
 TGTAAATATGATTTATACCTAACTGAATAAAAAGCTGTTCTGTCTTCCCNCCCA

42/75

## **FIGURE 42**

><MW: 14646, pI: 10.45, NX(S/T): 0

MAQSLALSLILVLAFGIPRTQGS D GGAQDCCLKYSQRKIPAKVVRSYRKQEP  
SLGCSI PAI  
LFLPRKRSQAELCADPKELWVQQLMQHLDKTPSPQKPAQGCRKDRGASKTGKKGKGS  
KGCKR  
TERSQTPKGP

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 67-71

**N-myristoylation sites.**

amino acids 17-23, 23-29, 27-33, 108-114, 118-124, 121-127

**Amidation site.**

amino acids 112-116

**Small cytokines.**

amino acids 51-91

## FIGURE 43

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC  
 CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTT  
 CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
 ACACCTTCCCAAATGTCACCTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
 GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA  
 TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCCTCTACA  
 TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
 AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
 ATCCCTGGGAGAGCTCGACGTCCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
 CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT  
 GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
 CACTGGCTGGCCTCAGGCTGTCTTATTCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
 TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
 CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
 GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

**FIGURE 44**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282  
><subunit 1 of 1, 177 aa, 1 stop  
><MW: 20452, pI: 8.00, NX(S/T): 2  
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSTFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

45/75

## FIGURE 45

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCCTGCCCGGGGCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGGAG  
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCC**ATG**CGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTGCCTCTGCGGACCGTGCCCATCAAGGG  
CGTGACACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAG**TAA**CT  
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTtagCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGTCCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGT

## **FIGURE 46**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
 RADGVVDCARGQSAHSLLEIKAVALLRTVAIKGVHVSRYLCMGADGKMQGLLQYSEEDCAFEE  
 EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
 MFSSPLETDSMDPFGLVTGLEAVRSPSEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

GTCTGTTCCAGGAGTCTCTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTTCTGAACC'TGAAGTCAGAATTCCCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTCATCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCCCTGGTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCC'TTTCCTACCACTGCTGAGTGGCCTGGAACTTGTTTAA  
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAC'TGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 48**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW  
KFDQGDTTTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPTMSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262



[illegible]

## **FIGURE 50**

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLGKPSGKSKDCVFTEIVLE  
NNYTAFQNRHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 51

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAGA  
AAAAAATC**ATG**AAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTT**TGA**TGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGACAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

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## **FIGURE 52**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV  
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

**Signal peptide:**

amino acids 1-28

[illegible]

amino acids 301-304

55/75

## **FIGURE 55**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC  
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT  
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
**ATAG**ACCGCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

56/75

## **FIGURE 56**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQGSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVG
LSA
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90



## FIGURE 57

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA

## **FIGURE 58**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
 SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
 SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ  
 WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
 VVAGAVVGTTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
 SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQPISP I PGGVSSSGLSR  
 MGAVPVMVPAQSQA GSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
 262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

59/75

## FIGURE 59

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGAGGCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT  
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCCCTGCAGAACTGCACAATGTACAGTGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC  
AATATTGAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC  
CACCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG  
CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA  
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTGCTGGCATATGCACAAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAATACAACCGGGGGCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTTAAATCTT

**FIGURE 60**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
 EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
 SRAALAQLLKLEELHLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
 VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
 LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
 PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMNLLSCPTTTPGLPLFTP  
 APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND  
 TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
 DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL  
 LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
 DFRLLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
 522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

61/75

62/75

## **FIGURE 62**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGVWNQFFVPEEMNTTSHH
IGQLRSDLNNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT
GRAVEPESEFVIKVSNDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL
LYSLLQGQPYFSVEPTTGIVIRISSKMDRELQDEYVWVIIQAKDMIGQPGALSGTTSVLIKLSD
VNDNKPIFKESLYRLTVSESAPTGTSGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR
DESIEEHFHYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP
SLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIIFGFIFLTLGLKQ
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY
RQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESASVSDQD
ESYDYLNELGPRFKRLACMFGSAVQSNN
```

**Important features:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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## **FIGURE 63**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCA**ATGGC**  
CGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTC  
TCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGTGCAGGCTTGAC  
AAGTCCAACCTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAG  
CTTGGCTGATAACAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTA  
TGAGTGAGCGCTGCTATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGCTGTTC  
CCTCAATCTGATAGGTTCCAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAG  
CAACAGGCTAAGCACATGTCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAA  
AGCTGAAGGACACAGTGAAAAAGCTTGGAGAGAGTGAGAGATCAAAGCAATTGGAGAACTG  
GATTTGCTGTTTATGTCTCTGAGAAATGCCTGCATT**TGACC**CAGAGCAAAGCTGAAAAATGAA  
TAACTAACCCCTTTCCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAAAC  
CAAAAGGAAGATGGGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGT  
TAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCA  
TAGATATTTATTGATAACATTTTCATTGTAAGTGGTGTCTATACACAGAAAACAATTTATTT  
TTTAAATAATTGTCTTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCC  
CTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTA  
TAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCG  
ATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAAC  
ATGTTTATTTGACCTCAATAAACACTTGGATATCCC

64/75

## **FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125185
><subunit 1 of 1, 179 aa, 1 stop
><MW: 20011, pI: 8.10, NX(S/T): 3
MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAAPISSHCRLDKSNFQQPYITNRTFMLAKE
ASLADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPPQSDRFQPYMQEVVPFLAR
LSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-33

#### **N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

#### **N-myristoylation sites.**

amino acids 14-20, 82-88

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21



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## FIGURE 65

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGA  
CGCGCGCCCTGCGTCGGGCGAAGAAAAGAAGCAAACTTGTTCGGGAGGGTTTCGTCATCAAC  
CTCCTTCCCGCAAACCTAAACCTCCTGCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCA  
GAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGCGCTGGCTGTGGAATTAGATCTGT  
TTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGCACCGGGTTGG  
CGCTGCCCCGAGTGGAAACGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCG  
GTTGTTGTTCAGTGTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAGAGAGCCTCAGAGG  
TCCGAAGAGCGCTGCGCTCCTACTCGCGTTTCGTTCTTCTCCTCTTCGGTTCCCTACTGTGA  
AATCGCAGCGACATTTACAAAGGCCTCCGGGTCTTACCGAGACCGATCCGCAGCGTTTGGCC  
CGGTCTGTCCTATTGCATCGGGAGCCCCCGAGCACCGGGCGAAATGGCGAGGTTCCCGAAGGC  
CGACCTGGCCGCTGCAGGAGTTATGTTACTTTGCCACTTCTTCACGGACCAGTTTTCAGTTTCG  
CCGATGGGAAACCCGGAGACCAATCCTTGATTGGCAGTATGGAGTTACTCAGGCCTTCCCT  
CACACAGAGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCACAGGTGGAAAAGAACTT  
GGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGAGCCCA  
GAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGAT  
ACAGACCACAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTT  
ATGGGTGAACATAGACCAAATGGAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATA  
CTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTTCGATTTTCCATTTTATGGCCACTTCCTA  
CGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGTCGTACATCGAATGCT  
AACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAATT  
CAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTC  
CAGGATAATTATAACCTGGGAAGCTTCACATTCCAGGCAACCCCTGCTCATGGATGGACGAAT  
CATCTTTGGATACAAAGAAATTCCTGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAG  
TGAAAGTCGGACTGTCCGATGCATTTGTCTGTTGTCCACAGGATCCAACAAATTCCCAATGTT  
CGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAAAATTACCAACAT  
TTCGGCTGTGGAGATGACCCCATTAACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTG  
TATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGG  
TTTGATCGTCATCGGCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGAT  
GTGTGAGAATACAGAACCAGTGGAAACTTCTTCTCGAACCACCACAACCGTAGGAGCGACAA  
CCACCCAGTTCAGGGTCCTAACTACCACCAGAAGAGCAGTGACTTCTCAGTTTCCCACCAGC  
CTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGCTTCTACAGA  
TGACAGTGCAGCTGAGAAGAAAGGGGGAACCCCTCCACGCTGGCCTCATCATTTGGAATCCTCA  
TCCTGGTCCCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACA  
TCAGCAGCCAGCATCTTCTTTATTGAGAGACGCCAAGCAGATGGCCTGCGATGAAGTTTAG  
AAGAGGCTCTGGACATCCTGCCTATGCTGAAGTTGAACCAGTTGGAGAGAAAGAAGGCTTTA  
TTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAACACCAGTACTGGTTTACAGGTGT  
TAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACACAAACAAGCTC  
TAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGG  
TAAACAAAAAACTAAACTTATACAAGATACCATTTTACTGAACATAGAATTCCCTAGTGG  
AATGTCATCTATAGTTCACTCGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTA  
TAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAGGGATCAGAAAAAAAATCATAATAAAGC  
TTTAGTTCATGAGGG

**FIGURE 66**

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEEEVEVD SHAYS  
 HRWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYIISRIYGPS  
 DSASRDLWVNIDQMEKDKVKI HGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTG  
 EVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQAT  
 LLMDGRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQ  
 MSKITNISAVEMTPLPTCLQFNRCGPCVSSQIGFNC SWCSKLQRCSSGFDRHRQDWVDSGCP  
 EESKEKMCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLK  
 DNGASTDDSAAEKKGGTLHAGLIIGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR  
 WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC

**Important features of the protein:****Transmembrane domain:**

amino acids 454-478

**N-glycosylation sites.**

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 297-301, 492-496, 503-507

**N-myristoylation sites.**

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,  
 455-461

GCAGCCCTAGCAGGAGATGACACATGATGCTGTTGGTGCAGGGTGCTTGTGCTCGAACCCAGTGGCTGGCGGGCGGTGCTCCTCAGCCTGTGCTGCCTGCTACCCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCCTGGGCGGCCGTGGACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTTGAAGATGGAGCTTCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGTGGATCCTCGAGTTTCAATTTCAACATTGAATAAAAAGGACTACAGCCTCCAGATACAGAATGTAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTCAGACTCAACATACACCCAGAACAAATGCAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGACCGTCAATGAAGGAACCAACGTCCTACTCTTACTTGTTGGCCACTGGGAAACCAGAGCCTTCCATTTCTTGCGCACACATCTCCCCATCAGCAAAACCAATTTGAAAATGGACAATATTTGGACATTTATGGAATTACAAGGGACCAGGCTGGGGAATATGATGTCAGTGCAGGAAAATGATGTGTCATTCCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTTCAGGAAATTAAATCTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCCTCCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTATTCAAATTTTAGCACAAAGATCCATTCTCACTGTTAACAACGTGACACAGGAGCACTTCGGCAATTATACTTGTGTGGCTGCCAACAAGCTAGGCACACCAATGCGAGCCTGCCTCTTAACCCTCCAAGTACAGCCCAGTATGGAATTACGGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCTTGTGTTGACACTGTCTCTTTACCAGCATATTCTACCTGAAGAATGCCATTCTACAATTAAATTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCTGGTACAGTTTGTTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCCTTCTGTAGAATTGCTCATTATGTAAATACTTTAATCTACTCTTTTTTTGATTAGCTACATTACCTTGTGAAGCAGTACACATTGTCCTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTTAGAGGATATTAATTGTGATTTTCATGTTTGTAATCTACAACCTTTTCAAAGCATTTCAGTCATGGTCTGCTAGGTTGCAGGCTGTAGTTTACAAAACGGAATATTGCAGTGAATATGTGATTCTTTAAGGCTGCAATACAAGCATTTCAGTTCCCTGTTTCAATAAGAGTCAATCCACATTTACAAAGATGCATTTTTTTCTTTTTTGATAAAAAAGCAAATAATATGCTTTCAGATTATTTCTTCAAATATAACACATATCTAGATTTTTCTGCTCGCATGATATTCAGGTTTCAGGAATGAGCCTTGTAATATAACTGGCTGTGCAGCTCTGCTTCTCTTTCCTGTAAAGTTCAGCATGGGTGTGCCCTTCATACAATAATATTTTTCTCTTGTCTCCAATAATATAAATGTTTTTGCTAAATCTTACAATTTGAAAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGCTATTGGACTGTAAAAATCTCTTCCCTGCACTGACAAAGGGGTTTGAGAATTTTGCCCCACACTAACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCTTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAATCATTCCCTTTAAATGACAGCACAGTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCTTTTCACTAGTCCAAGCCAAAAATTTTAAGATGATTTGTCAGAAAGGGCACAAAGTCCATCACCTAATATTACAAGAGTTGGTAAGCGCTCATCATTATTTTATTTTGTGGCAGCTAAGTTAGTAGATGACAGAGGCAGTGCTCCTGTGGACAGGAGCATTTTGCATATTTTCCATCTGAAAGTATCACTCAGTTGATAGTCTGGAATGCATGTTATATATTTTAAACCTCCAAAATATATTAACAAACATTTCTATATCGGTATGTAGCAGACCAATCTCTAAAATAGCTAATTTCTTCAATAAATCTTTCTATATAGCCATTTTCAGTGCAACAAGTAAAAACAAAAGACCATCTTTATTTTCTCTTACATGATATATGTAAGATGCGATCAAATAAAGACAAAACACCAGTGATGAGAAATCTTAAGATAAGTAATTATCAAATTATTGTGAATGTTAAATTATTTCTACTATAAAGAAGCAAACCTACATTTTTTGAAGGAAAATGCTGTTACTCTAACATTAATTTACAGGAATAGTTTGATGGTTTCACTCTTTACTAAAGAAAGGCCATCACCTTGAAAGCCATTTTACAGGTTTGATGAAGTTACCAATTTTCAGTACACCTAAATTTCTACAAATAGTCCCCTTTTACAAGTTGTAACAACAAAGACCCTATAATAAAATTAGATACAAGAAATTTTGCAGTGGTTATACATATTTGAGATATCTAGTATGTTGCCCTAGCAGGGATGGCTTAAAAACTGTGATTTTTTTTTCTTCAAGTAAAACCTTAGTCCCAAAGTACATCATAAATCAATTTTAATTAGAAAAATGAATCTTAAATGAGGGGACATAAGTATACTCTTTCCACAAAATGGCAATAATAAGGCATAAAGCTAGTAAATCTACTAACTGTAATAAATGTATGACATTATTTTGATTGATACATTAAAAAAGAGTTTTTGAACAAATATGGCATTAACTTTTATTATTTATTTTGCTTTTAAGAAATATTCTTTGTGGAATTGTTGAATAAACTATAAATATTATTTTGTTATTGCAGCTTTAAAGTGGCACACTCCATAATAATCTACTTACTAGAAAT

## FIGURE 67B

AGTGGTGCTACCACAAAAAATGTTAACCATCAGTACCATTGTTTGGGAGAAAGAAACAGATC  
AAGAATGCATATTATTTCAGTGACCGCTTTCCTAGAGTTAAAATACCTCCTCTTTGTAAGGTT  
TGTAGGTAAATTGAGGTATAAACTATGGATGAACCAATAATTAGTTCAAAGTGTTGTCATG  
ATTCCAAATTTGTGGAGTCTGGTGTTTTTACCATAGAATGTGACAGAAGTACAGTCATAGCT  
CAGTAGCTATATGTATTTGCCTTTATGTTAGAAGAGACTTTCCTTGAGTGACATTTTTTAAATA  
GAGGAGGTATTCACATATGTTTTTCTGTATCACAGCAGCATTCCTAGTCCTTAGGCCCTCGGA  
CAGAGTGAAATCATGAGTATTTATGAGTTCAATATTGTCAAATAAGGCTACAGTATTTGCTT  
TTTTGTGTGAATGTATTGCATATAATGTTCAAGTAGATGATTTTACATTTATGGACATATAA  
AATGTCTGATTACCCCATTTTATCAGTCCTGACTGTACAAGATTGTTGCAATTTTCAGAATAG  
CAGTTTTATAAATTGATTTATCTTTTAATCTATAACAATTTGTGTTAGCTGTTTCATTTTCAGG  
ANTATATTTTCTACAAGTTCCACTTGTGGGACTCCTTTTGTGCCCCCTATTTTTTTTTTAAAG  
AAGGAAGAAAGAAAAATAAGTAGCAGTTTAAAAATGAGAATGGAGAGAAAAGAAAAAGAATG  
AAAAGGAAAGGCAGTAAAGAGGGAAAAAAAAGGAAGGATGGAAGGAATGAAGGAAGGAAGGG  
AGGAAGGGGAGAAGGTAGGAAGAAAGAAAGGATGAGAGGGGAAGGAAGAATCAGAGTATTAGG  
GTAGTTAACTTACACATTTGCATTCTTAGTTTAACTGCAAGTGGTGTAAGTATGTTTTTCAA  
TGATCGCATTTGAAACATAAGTCCTATTATACCATTAAAGTTCCTATTATGCAGCAATTATAT  
AATAAAAAGTACTGCCCAAGTTATAGTAATGTGGGTGTTTTTTGAGACACTAAAAGATTTGAG  
AGGGAGAATTTCAAACCTTAAAGCCACTTTTGGGGGGTTTATAACTTAACTGAAAAATTAATG  
CTTCATCATAACATTTAAGCTATATCTAGAAAGTAGACTGGAGAACTGAGAAAATTACCCAG  
GTAATTCAGGGAAAAAAAATATATATATATATAAATACCCCTACATTTGAAGTCAGAAA  
ACTCTGAAAACTGAATTATCAAAGTCAATCATCTATAATGATCAAATTTACTGAACAATTG  
TTAATTTATCCATTGTGCTTAGCTTTGTGACACAGCCAAAAGTTACCTATTTAATCTTTTCA  
ATAAAAATTGTTTTTTGAAATCCAGAAATGATTTAAAAAGAGGTCAGGTTTTTAACTATTTA  
TTGAAGTATGTGGATGTACAGTATTTCAATAGATATGAATATGAATAAATGGTATGCCTTAA  
GATTCTTTGAATATGTATTTACTTTAAAGACTGGAAAAAGCTCTTCCTGTCTTTTAGTAAAA  
CATCCATATTTCATAACCTGATGTAAAATATGTTGTACTGTTTCCAATAGGTGAATATAAAC  
TCAGTTTATCAATTAAAAA

**FIGURE 68**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92259
><subunit 1 of 1, 354 aa, 1 stop
><MW: 38719, pI: 6.12, NX(S/T): 6
MDMMLLVQGACCSNQWLAHAVLLSLCCLLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYL
EDGASKGAWLNRSSIIIFAGGDKWSVDPRVSISTLNKR DYS LQIQNV DVTDDGPYTCSVQTQH
TPRTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQ
YLDIYGITRDQAGEYEC SAENDVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGA
GVPPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASL
PLNPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 322-343

**N-glycosylation sites.**

amino acids 73-77, 155-159, 275-279, 286-290, 294-298, 307-311

**Tyrosine kinase phosphorylation site.**

amino acids 180-188

**N-myristoylation sites.**amino acids 9-15, 65-71, 69-75, 153-159, 241-247, 293-299,  
304-310, 321-327**Myelin P0 protein.**

amino acids 94-123

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## **FIGURE 69**

ATAGTAGAAGAATGTCTCTGAAATTACTGGATGAGTTTCAGTCATACTTTCACATGGGCACA  
ATTTACATTCAAGCTCCTTATCCTAGGCTAATTTTATATTATGTTAAATCACTTGTTTTTG  
TTCTCACGGCTTCCTGCCTGCTATAGGCATAATTACGAGGAAGCAGAACTTCTCCAGAAGCA  
AGCGCACATGCGTTCCAAAATAAGAGCAAATTCGCTCTAAACACAGGAAAAGACCTGAAGCT  
TTAATTAAGGGGTACATCCAACCCAGAGCGCTTTTGTGGGCACTGATTGCTCCAGCTTCT  
GCGTCACTGCGCGAGGGAAGAGGGAAGAGGATCCAGGCGTTAGAC**ATG**TATAGACACAAAA  
CAGCTGGAGATTGGGCTTAAATAACCCACCAAGCTCCAAAGAAGAGACCCAAGTCCCCAAAA  
CATTGATTTTCAGGGCTGCCAGGAAGGAAGAGCAGCAGCAGGGTGGGAGAGAAGCTCCAGTCA  
GCCCACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCAC  
CGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG  
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAG  
GCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGC  
ACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCT  
TCTCCTCCTGCAAA**TAG**

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## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA44175

><subunit 1 of 1, 155 aa, 1 stop

><MW: 17194, pI: 10.44, NX(S/T): 0

MYRHKNSWRLGLKYPPSSKEETQVPKTLISGLPGRKSSSRVGEKLQSAHKMPLSPGLLLLLL  
SGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEAREVA  
RRQEGAPPQQSARRDRMPCRNFFWKTFSSCK

### **Important features of the protein:**

#### **Transmembrane domain:**

amino acids 51-69

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 35-39, 92-96

#### **N-myristoylation sites.**

amino acids 64-70, 75-81, 90-96

#### **Amidation site.**

amino acids 33-37

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## FIGURE 71

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GCGTGGAGCCTTGGGA  
GCTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTC  
AGAATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGG  
GAACCTGACTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATA  
CTACCTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTC  
AGGGCTGAATTTGCAGATGAGCATTGAGCTGGGTAAACATCACCTTCTGTCTGTGGATGA  
CACCATTATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTT  
TCTTAGCCCCCTAAAATTGAGAATGAATACGAAACTTGGACTATGAAGAATGTGTATAACTCA  
TGGACTTATAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCA  
GTATGACTTTTGAGGTCCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAG  
GGTTTCTTCCTGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACC  
CATGACGAAACGGTCCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGT  
CTGCCTGGCACTCCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACG  
CCTTCTCCCCCTAGGAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCAT  
AACACACTTCTGTTTTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAG  
TGTCATTGCAGAAGACTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGA  
CCCCGCCTGGGCAGGGGCCCCAAAGC**TAG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACA  
GTGACGTACTCCATCTCACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGA  
CCATCTGAGCCAGCCCCACATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACAT  
TTTAAAGGCTGTCTTGGCAAAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCA  
TGATGTTTTTCAGAAGTTGGCCACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAA  
GATCATGTTTTAATTGTGAGAAACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCA  
CCTTAGAGGTCGAGGCAGGCGGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAATA  
TGGTGAAACCCAGTCTCTACTAAAAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTAT  
AATCCCAGCTACTCGAGTGCCTGAGGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGA  
GGTTGCAGTGAGCCGAGATAGCGGCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCAT  
CTCAAAAAAAAAAAAAAAAAAATTGTGAGAAACAGAAATACTTAAATGAGGAATAAGAATGG  
AGATGTTACATCTGGTAGATGTAACATTCTACCAGATTATGGATGGACTGATCTGAAAATCG  
ACCTCAACTCAAGGGTGGTCAGCTCAATGCTACACAGAGCACGGACTTTTGGATTCTTTGCA  
GTACTTTGAATTTATTTTTCTACCTATATATGTTTTATATGCTGCTGGTGCCTCCATTAAAGT  
TTTACTCTGTGTTGC



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## **FIGURE 72**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIF
QDKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLA
DSLHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTT
YCVQVRGFLPDRNKAGEWSEPVCEQTTTHDETVPSPWMVAVILMASVFMVCLALLGCFSLWLVCV
YKKTKYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPNG
DSCSLGTTPPGQGPQS

```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 222-245

#### **N-glycosylation sites.**

amino acids 49-53, 68-72, 102-106, 161-165

#### **N-myristoylation sites.**

amino acids 6-12, 316-322

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## FIGURE 73

CGAGCGCCAACCCGCTAGCGCCTGAATCCGGCGTGCTGCCCGCTCGCCGCCCGGCC**ATGG**CCCC  
GCGCAGCCCCGCTGCTCGCCGCGTTGACCGCGCTCCTCGCCGCCGCCGCTGCTGGCGGAGAT  
GCCCCGCCGGGCAAAATCGCGGTGGTTGGGGCTGGGATTGGGGGCTCTGCTGTGGCCCATTT  
TCTCCAGCAGCACTTTGGACCTCGGGTGAGATCGACGTGTACGAGAAGGGAACCGTGGGTG  
GCCGCTTGGCCACCATCTCAGTCAACAAGCAGCACTATGAGAGCGGGGCTGCCTCCTTCCAC  
TCCCTGAGCCTGCACATGCAGGACTTCGTCAAGCTGCTGGGGCTGAGGCACCGGCGCGAGGT  
GGTGGGCAGGAGCGCCATCTTCGGCGGGGAGCACTTCATGCTGGAGGAGACTGACTGGTACC  
TGCTGAACCTCTTCCGCCTCTGGTGGCACTATGGCATCAGCTTCCTGAGGCTGCAGATGTGG  
GTGGAGGAGGTTCATGGAGAAGTTCATGAGGATCTATAAGTACCAGGCCACGGCTATGCCTT  
CTCGGGTGTGGAGGAGCTGCTCTACTCACTGGGGGAGTCCACCTTTGTAAACATGACCCAGC  
ACTCTGTGGCTGAGTCCCTGCTGCAGGTGGGCGTCACGCAGCGCTTTATTGATGATGTGCTT  
TCTGCTGTCTTGCGGGCCAGCTATGGCCAGTCAGCAGCGATGCCCGCCTTTCAGGAGCCAT  
GTCCTAGCCGGGGGCCCAAGGCAGCCTGTGGTCTGTGGAAGGAGGCAATAAGCTGGTTTGT  
CCGGTTTGTGAAGCTCACCAAGGCCAATGTGATCCATGCCACAGTGACCTCTGTGACCCTG  
CACAGCACAGAGGGGAAAGCCCTGTACCAGGTGGCGTATGAGAATGAGGTAGGCAACAGCTC  
TGACTTCTATGACATCGTGGTCATCGCCACCCCCCTGCACCTGGACAACAGCAGCAGCAACT  
TAACCTTTGCAGGCTTCCACCCGCCCATTTGATGACGTGCAGGGCTCTTTCCAGCCCACCGTC  
GTCTCCTTGGTCCACGGCTACCTCAACTCGTCCTACTTCGGTTTCCAGACCCTAAGCTTTT  
CCCCTTTGCCAACATCCTTACCACAGATTTCCCCAGCTTCTTCTGCACTCTGGACAACATCT  
GCCCTGTCAACATCTCTGCCAGCTTCCGGCGAAAGCAGCCCCAGGAGGCAGCTGTTTGGCGA  
GTCCAGTCCCCCAAGCCCCTCTTTCGGACCCAGCTAAAGACCCTGTTCCGTTCCTATTACTC  
AGTGCAGACAGCTGAGTGGCAGGCCCATCCCCTCTATGGCTCCCGCCCCACGCTCCCGAGGT  
TTGCACTCCATGACCAGCTCTTCTACCTCAATGCCCTGGAGTGGGCGGCCAGCTCCGTGGAG  
GTGATGGCCGTGGCTGCCAAGAATGTGGCCTTGCTGGCTTACAACCGCTGGTACCAGGACCT  
AGACAAGATTGATCAAAAAGATTTGATGCACAAGGTCAAGACTGAACTGTGAGGGCTCTAGG  
GAGAGCCTGGGAACTTTTCATCCCCCACTGAAGATGGATCATCCCACAGCAGCCCAGGACTGA  
ATAAGCCATGCTCGCCCACCAGGCTTCTTTCTGACCCCTCATGTATCAAGCATCTCCAGGTG  
ACCTACTGTCTGCCTATATTAAGGGTCCACACGGCGGCTGCTGCTTTTTTTTTTAAGGGGGAAA  
GTAAGAAAAGAGAAGGAAATCCAAGCCAGTATATTTGTTTATTTATTTTAAAGAAGAA  
AAAAGTTCATCTTCACAAGGTGCTTCAGACTTGGTTTCTTAGCTAGAAACCAGAAGACTACG  
GGAGGGAATATAAGGCAGAGAACTATGAGTCTTATTTTATTACTGTTTTTCACTACCTACTC  
CCACAATGGACAATCAATTGAGGCAACCTACAAGAAAACATTTACAACCAGATGGTTACAAA  
TAAAGTAGAAGGGAAGATCAGAAAACCTAAGAAATGATCATAGCTCCTGGTTACTGTGGACT  
TGATGGATTTGAAGTACCTAGTTCAGAACTCCCTAGTCACCATCTCCAAGCCTGTCAACATC  
ACTGCATATTGGAGGAGATGACTGTGGTAGGACCCAAGGAAGAGATGTGTGCCTGAATAGTC  
GTCACCATATCTCCAAGCTTCTTGGCAACCAGTGGGAAAAGAAACATGCGAGGCTGTAGGAA  
GAGGGAAGCTCTTCTTGGCACCTAGAGGAATTAGCCATTCTCTTCCTTATGCAAAGATTGA  
GGAATGCAACAATATAAAGAAGAGAAGTCCCCAGATGGTAGAGAGCAGTCATATCTTACCCC  
TAGATGTTTCATCCCAGCAGAAGAAAGAAGGTGTTGGGGTAGGATTCTTCAGAGGTTAGC  
CTGGTACTTTCTCATCAGACACTAGCTTGAAGTAAGAGGAGAATTATGCTTTTCTTTGCTTT  
TTCTACAAACCCTTAAAAATCACTTGTTTTAAAAAGAAAGTAAAGCCCTTTTCATTCAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 74**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA116510

><subunit 1 of 1, 494 aa, 1 stop

><MW: 54646, pI: 7.27, NX(S/T): 6

MARAAPLLAALTALLAAAAAGGDAPPGKIAVVGAGIGGSAVAHFLQQHFGPRVQIDVYEKGT  
VGGRLATISVNKQHYESGAASFHSLSLHMQDFVKLLGLRHRREVVGSAIFGGEHFMLEETD  
WYLLNLFRLWWHYGISFLRLQMWWVEEVMEKFMRIYKYQAHGYAFSGVEELLYSLGESTFVNM  
TQHSVAESLLQVGVVTQRFIDDVVSAVLRASYGQSAAMPAFAGAMSLAGAQQSLWSVEGGNKL  
VCSGLLKLTKANVIHATVTSVTLHSTEGKALYQVAYENEVGNSSDFYDIVVIATPLHLDNSS  
SNLTFAGFHPPIDDVQGSFQPTVVSLSVHGYNSSYFGFPDPKLFPPFANILTTDFPSFFCTLD  
NICPVNISASFRRKQPQEAAVWRVQSPKPLFRTQLKTLFRSYYSVQTAEWQAHPLYGSRPTL  
PRFALHDQLFYLNLEWAASSVEVMAVAANKVALLAYNRWYQDLDKIDQKDLMHKVKTTEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **N-glycosylation sites.**

amino acids 185-189, 290-294, 308-312, 312-316, 342-346, 378-382

#### **N-myristoylation sites.**

amino acids 33-39, 35-41, 38-44, 61-67, 64-70, 218-224, 234-240,  
237-243, 429-435